

Amendments to the Claims:

This listing of claims replaces all prior versions and listings of claims in the application:

Listing of Claims:

1-18. (Cancelled)

19. (Presently Amended) An antibody or an antigen binding fragment thereof ~~having comprising the~~ a complementarity determining region-H3 (CDR-H3) ~~CDR-H3~~ sequence selected from the group consisting of: SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 30, and SEQ ID NO: 31.

20. (Presently Amended) An antibody or an antigen binding fragment thereof ~~having comprising the~~ a complementarity determining region-L3 (CDR-L3) ~~CDR-H3~~ sequence selected from the group consisting of: SEQ ID NO: 32, SEQ ID NO: 33 and SEQ ID NO: 34.

21. (Presently Amended) An antibody or an antigen binding fragment thereof ~~having comprising a~~ complementarity determining region-H3 (CDR-H3) ~~CDR-H3~~ sequence selected from the group consisting of: SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 30, and SEQ ID NO: 31 and a complementarity determining region-L3 (CDR-L3) ~~CDR-L3~~ sequence selected from the group consisting of: SEQ ID NO: 32, SEQ ID NO: 33 and SEQ ID NO: 34.

22. (Presently Amended) A method for identifying candidate antigen-specific sequences ~~of at least the CDR3 region~~ of antibodies specific against at least one antigen produced by *Clostridium difficile*, ~~during an infection or against a vaccine~~, the method comprising ~~the steps~~ of:

(i) ~~with B cells isolated from at least one patient who has been infected by *Clostridium difficile* or administered said vaccine, obtaining B cells from at least one patient whose immune system has been exposed to the antigen and sequencing from the B-cells at least the complementarity determining region-3 (CDR3) regions of CDR3-region of the of the VH and/or VL variable heavy chains (VH) or variable light chains (VL), or both regions of said B cells; and~~

(ii) ~~correlating said sequences of at least the CDR3 regions of the VH and/or VL coding regions of said B cells from said at least one patient to identify detecting a set of candidate sequences for at least a CDR3-region that occur in total at a frequency of at least one percent of antibodies specific against said at least one antigen produced by *Clostridium difficile* or against said vaccine, wherein the each of said set of candidate CDR3 sequences include a dominant sequence and sequences or a sequence having of at least 80% homology to the dominant sequence. therewith occurring in total at a frequency of at least 1 percent in the set of sequences determined at step (i).~~

23. (Presently amended) [[A]] ~~The method according to of claim 22, said wherein the B cells are being selected from the group consisting of peripheral B-cell lymphocytes or and B cells from the spleen.~~

24. (Presently amended) [[A]] ~~The method according to of claim [[23]] 22, said peripheral B-cell lymphocytes being wherein the B cells are isolated from blood from said at least one patient.~~

25. (Presently amended) [[A]] ~~The method according to of claim 22, said at least one wherein the antigen being is an immunogen.~~

26. (Presently amended) [[A]] The method according to of claim 22, said at least one wherein the patient displays displaying a pronounced antibody response in response to infection by *Clostridium difficile*.

27. (Presently amended) [[A]] The method according to of claim 22, said at least one patient having wherein the patient has recovered from infection by *Clostridium difficile*.

28. (Presently amended) [[A]] The method according to of claim 22, said correlation wherein step (i) comprises sequencing DNA or RNA from the B cells and step (ii) comprises comprising determining putative amino acid sequences based on the DNA or RNA sequences sequenced regions from said sequences of at least the VH and/or VL CDR3 coding regions, and wherein the set of sequences is detected among the correlating said putative amino acid sequences.

29. (Presently amended) [[A]] The method according to of claim [[27]] 22, said correlation wherein step (ii) further comprises comprising identifying CDR2 regions and detecting a set of candidate sequences among the CDR2 regions the Complementarity Determining Regions in said at least the VH and/or VL regions and correlating said Complementarity Determining Regions.

30. (Presently amended) [[A]] The method according to of claim 29, wherein step (ii) further comprises identifying CDR1 regions and detecting a set of candidate sequences among the CDR1 regions said Complementarity Determining Regions being selected from the group consisting of CDR1, CDR2 and CDR3.

31. (Presently amended) [[A]] The method according to of claim 22, said correlation wherein step (ii) additionally correlating at least one of the group consisting of: further comprises determining at least one factor from the group consisting of: the strain of *Clostridium difficile*

~~infecting the patient; infecting said at least one patient, the time point at which said the B cells are isolated during infection; of said at least one patient by *Clostridium difficile*, and the age of said at least one the patient;[,]~~ the sex ~~of said at least one the patient;[,]~~ and the race of ~~said at least one the patient;[,]~~ and correlating the factor with the candidate sequence.

32. (Presently amended) [[A]] The method according to of claim 22, wherein the  
~~said B cells having been~~ are isolated from ~~the said at least one patient~~ at a plurality of time points during infection of ~~said at least one patient by *Clostridium difficile*, said correlation step (ii) correlating the time point during infection of said at least one patient by *Clostridium difficile* at which said B cells are isolated.~~

33. (Presently amended) [[A]] The method of claim 22, said wherein the B cells  
~~having been~~ are isolated from at least two patients, ~~at least one of whom has recovered from infection by from *Clostridium difficile*, and at least one of whom has not recovered from infection by *Clostridium difficile*, and wherein sequences from the recovered patient are compared with sequences from the patient who has not recovered to identify sequences that are not effective to clear the infection said correlation step (ii) correlating the recovery of said at least two patients from infection by *Clostridium difficile*.~~

34. (Presently amended) [[A]] The method according to of claim 22, said wherein  
~~the B cells having been~~ are isolated from at least two patients, ~~said wherein each patient patients being has been~~ infected by a strain ~~different strains of *Clostridium difficile* different from the strain that has infected the other producing said at least one antigen, said correlation and wherein sequences from one patient are compared with sequences from the other patient step (ii) further correlating said sequence of at least the VH and/or or VL coding regions of said B cells to identify a set of candidate sequences for antibodies, each of which is specific against at least one shared antigen produced by said the different strains of *Clostridium difficile* or is specific against different antigens produced by said different strains of *Clostridium difficile*.~~

35. (Presently amended) A method of producing a database which identifies candidate sequences for antibodies specific against at least one antigen produced ~~produces~~ by *Clostridium difficile*, comprising the steps of:

- (i) performing [[a]] the method according to claim 22; and
- (ii) storing the data produced by said method in the ~~said~~ database.

36. (Presently amended) A method of generating a report which identifies candidate sequences for antibodies specific against at least one antigen produced by *Clostridium difficile*, comprising the steps of:

- (i) performing [[a]] the method according to claim 22; and
- (ii) producing a report comprising the data produced by the ~~said~~ method.

37. (New) A method for treating an infection by *Clostridium difficile* in a patient, the method comprising administering to the patient a pharmaceutically effective amount of the antibody or the antigen binding fragment thereof of claim 19.

38. (New) A method for treating an infection by *Clostridium difficile* in a patient, the method comprising administering to the patient a pharmaceutically effective amount of the antibody or the antigen binding fragment thereof of claim 20.

39. (New) A method for treating an infection by *Clostridium difficile* in a patient, the method comprising administering to the patient a pharmaceutically effective amount of the antibody or the antigen binding fragment thereof of claim 21.